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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=5; day=1; hr=15; min=18; sec=40; ms=565;]

=====

Reviewer Comments:

<210> 40

<211> 374

<212> PRT

<213> *Pichia pastoris*

<220>

<221> MOD_RES

<222> (176)...(190)

<223> Variable amino acid

<220>

<221> MOD_RES

<222> (202)...(213)

<223> Variable amino acid

<400> 40

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Ile	Arg	Gln	Gly	Glu	Leu	Asp	Tyr	Ser	Asn	Ile	Phe	Gly	Asp	Thr	Gly
			20					25					30		
Pro	Leu	Val	Tyr	Pro	Ala	Gly	His	Val	His	Ala	Tyr	Ser	Val	Leu	Ser
		35					40					45			
Trp	Tyr	Ser	Asp	Gly	Gly	Glu	Asp	Val	Ser	Phe	Val	Gln	Gln	Ala	Phe
	50					55				60					
Gly	Trp	Leu	Tyr	Leu	Gly	Cys	Leu	Leu	Leu	Ser	Ile	Ser	Ser	Tyr	Phe
65					70				75					80	
Phe	Ser	Gly	Leu	Gly	Lys	Ile	Pro	Pro	Val	Tyr	Phe	Val	Leu	Leu	Val
			85					90					95		
Ala	Ser	Lys	Arg	Leu	His	Ser	Ile	Phe	Val	Leu	Arg	Leu	Phe	Asn	Asp

			100					105					110			
Cys	Leu	Thr	Thr	Phe	Leu	Met	Leu	Ala	Thr	Ile	Ile	Ile	Leu	Gln	Gln	
			115					120					125			
Ala	Ser	Ser	Trp	Arg	Lys	Asp	Gly	Thr	Thr	Ile	Pro	Leu	Ser	Val	Pro	
			130					135					140			
Asp	Ala	Ala	Asp	Thr	Tyr	Ser	Leu	Ala	Ile	Ser	Val	Lys	Met	Asn	Xaa	
145					150					155					160	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Asp	
				165					170					175		
Glu	Asn	Leu	Ile	Lys	Ala	Leu	Ala	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
			180					185						190		
Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Ser	Phe	Ile	Leu	Pro	Leu	His	Tyr	Asp	Asp	
			195				200						205			
Gln	Ala	Asn	Glu	Ile	Arg	Ser	Ala	Tyr	Phe	Arg	Gln	Ala	Phe	Asp	Phe	
			210				215					220				
Ser	Arg	Gln	Phe	Leu	Tyr	Lys	Trp	Thr	Val	Asn	Trp	Arg	Phe	Leu	Ser	
225					230					235					240	
Gln	Glu	Thr	Phe	Asn	Asn	Val	His	Phe	His	Gln	Leu	Leu	Phe	Ala	Leu	
			245					250						255		
His	Ile	Ile	Thr	Leu	Val	Leu	Phe	Ile	Leu	Lys	Phe	Leu	Ser	Pro	Lys	
			260					265						270		
Asn	Ile	Gly	Lys	Pro	Leu	Gly	Arg	Phe	Val	Leu	Asp	Ile	Phe	Lys	Phe	
		275					280					285				
Trp	Lys	Pro	Thr	Leu	Ser	Pro	Thr	Asn	Ile	Ile	Asn	Asp	Pro	Glu	Arg	
		290				295						300				
Ser	Pro	Asp	Phe	Val	Tyr	Thr	Val	Met	Ala	Thr	Thr	Asn	Leu	Ile	Gly	
305					310					315					320	
Val	Leu	Phe	Ala	Arg	Ser	Leu	His	Tyr	Gln	Phe	Leu	Ser	Trp	Tyr	Ala	
			325					330						335		
Phe	Ser	Leu	Pro	Tyr	Leu	Leu	Tyr	Lys	Ala	Arg	Leu	Asn	Phe	Ile	Ala	
			340					345					350			
Ser	Ile	Ile	Val	Tyr	Ala	Ala	His	Glu	Tyr	Cys	Trp	Leu	Val	Phe	Pro	
		355					360					365				
Ala	Thr	Glu	Gln	Ser	Ser											
			370													

The above <222> responses describing Xaa locations are incorrect: Xaa is located at positions 160-174 and 186-197, not at locations 202-213.

Application No: 10500240

Version No: 3.0

Input Set:

Output Set:

Started: 2008-04-15 16:02:05.595

Finished: 2008-04-15 16:02:13.772

Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 177 ms

Total Warnings: 33

Total Errors: 53

No. of SeqIDs Defined: 106

Actual SeqID Count: 106

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2008-04-15 16:02:05.595
Finished: 2008-04-15 16:02:13.772
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 177 ms
Total Warnings: 33
Total Errors: 53
No. of SeqIDs Defined: 106
Actual SeqID Count: 106

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (24)
E 257	Invalid sequence data feature in <221> in SEQ ID (24)
E 257	Invalid sequence data feature in <221> in SEQ ID (26)
E 257	Invalid sequence data feature in <221> in SEQ ID (36)
E 257	Invalid sequence data feature in <221> in SEQ ID (36)
E 257	Invalid sequence data feature in <221> in SEQ ID (38)
E 257	Invalid sequence data feature in <221> in SEQ ID (38)
E 257	Invalid sequence data feature in <221> in SEQ ID (40)
E 257	Invalid sequence data feature in <221> in SEQ ID (40)
E 341	'Xaa' position not defined SEQID (40) POS (160)
E 341	'Xaa' position not defined SEQID (40) POS (161)
E 341	'Xaa' position not defined SEQID (40) POS (162)
E 341	'Xaa' position not defined SEQID (40) POS (163)
E 341	'Xaa' position not defined SEQID (40) POS (164)
E 341	'Xaa' position not defined SEQID (40) POS (165)
E 341	'Xaa' position not defined SEQID (40) POS (166)
E 341	'Xaa' position not defined SEQID (40) POS (167)
E 341	'Xaa' position not defined SEQID (40) POS (168)
E 341	'Xaa' position not defined SEQID (40) POS (169)
E 341	'Xaa' position not defined SEQID (40) POS (170)
E 341	'Xaa' position not defined SEQID (40) POS (171)

Input Set:

Output Set:

Started: 2008-04-15 16:02:05.595
Finished: 2008-04-15 16:02:13.772
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 177 ms
Total Warnings: 33
Total Errors: 53
No. of SeqIDs Defined: 106
Actual SeqID Count: 106

Error code	Error Description
E 341	'Xaa' position not defined SEQID (40) POS (172)
E 341	'Xaa' position not defined SEQID (40) POS (173)
E 341	'Xaa' position not defined SEQID (40) POS (174)
E 341	'Xaa' position not defined SEQID (40) POS (191)
E 341	'Xaa' position not defined SEQID (40) POS (192)
E 341	'Xaa' position not defined SEQID (40) POS (193)
E 341	'Xaa' position not defined SEQID (40) POS (194)
E 341	'Xaa' position not defined SEQID (40) POS (195) This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (42)
E 257	Invalid sequence data feature in <221> in SEQ ID (42)
W 402	Undefined organism found in <213> in SEQ ID (44)
W 402	Undefined organism found in <213> in SEQ ID (45)
W 402	Undefined organism found in <213> in SEQ ID (46)
W 402	Undefined organism found in <213> in SEQ ID (48)
E 257	Invalid sequence data feature in <221> in SEQ ID (54)
E 257	Invalid sequence data feature in <221> in SEQ ID (56)
E 257	Invalid sequence data feature in <221> in SEQ ID (58)
E 257	Invalid sequence data feature in <221> in SEQ ID (60)
E 257	Invalid sequence data feature in <221> in SEQ ID (62)
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E 257	Invalid sequence data feature in <221> in SEQ ID (72)

Input Set:

Output Set:

Started: 2008-04-15 16:02:05.595
Finished: 2008-04-15 16:02:13.772
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 177 ms
Total Warnings: 33
Total Errors: 53
No. of SeqIDs Defined: 106
Actual SeqID Count: 106

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (78) This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (86)
W 402	Undefined organism found in <213> in SEQ ID (87)
W 402	Undefined organism found in <213> in SEQ ID (88)
W 402	Undefined organism found in <213> in SEQ ID (90)
W 402	Undefined organism found in <213> in SEQ ID (92)
W 402	Undefined organism found in <213> in SEQ ID (94)

SEQUENCE LISTING

<110> WILDT, Stefan
MIELE, Robert G.
NETT, Juergen H.
DAVIDSON, Robert C.

<120> METHODS TO ENGINEER MAMMALIAN-TYPE
CARBOHYDRATE STRUCTURES

<130> GF0022P

<140> 10500240
<141> 2005-03-23

<150> PCT/US02/41510
<151> 2002-12-24

<150> 60/344,169
<151> 2001-12-27

<160> 106

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<220>
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<220>
<223> Primer

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<220>

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<400> 10

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<210> 11

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<210> 19	
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 <220>
 <223> Primer

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 <210> 23
 <211> 4
 <212> PRT
 <213> Saccharomyces cerevisiae

 <400> 23
 His Asp Glu Leu
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 <210> 24
 <211> 458
 <212> PRT
 <213> Saccharomyces cerevisiae

<220>
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<222> (304)...(318)
<223> Variable amino acid

<220>
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<222> (416)...(436)
<223> Variable amino acid

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20 25 30
Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
35 40 45
Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
50 55 60
Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
65 70 75 80
Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
85 90 95
Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
100 105 110
Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
115 120 125
Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
130 135 140
Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
145 150 155 160
Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
165 170 175
Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
180 185 190
Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
195 200 205
Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
210 215 220
Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
225 230 235 240
Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
245 250 255
Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
260 265 270
His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
275 280 285
Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe Xaa
290 295 300
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Val
305 310 315 320
Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
325 330 335
Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
340 345 350
Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
355 360 365

Ser	Leu	His	Tyr	Gln	Phe	Leu	Ser	Trp	Tyr	His	Trp	Thr	Leu	Pro	Ile
370						375					380				
Leu	Ile	Phe	Trp	Ser	Gly	Met	Pro	Phe	Phe	Val	Gly	Pro	Ile	Trp	Tyr
385					390					395					400
Val	Leu	His	Glu	Trp	Cys	Trp	Asn	Ser	Tyr	Pro	Pro	Asn	Ser	Gln	Xaa
				405					410					415	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				420					425					430	
Xaa	Xaa	Xaa	Xaa	Ser	Gly	Ser	Val	Ala	Leu	Ala	Lys	Ser	His	Leu	Arg
				435				440						445	
Thr	Thr	Ser	Ser	Met	Glu	Lys	Lys	Leu	Asn						
				450				455							

<210> 25

<211> 458

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 25

Met	Glu	Gly	Glu	Gln	Ser	Pro	Gln	Gly	Glu	Lys	Ser	Leu	Gln	Arg	Lys
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Gln	Phe	Val	Arg	Pro	Pro	Leu	Asp	Leu	Trp	Gln	Asp	Leu	Lys	Asp	Gly
			20					25					30		
Val	Arg	Tyr	Val	Ile	Phe	Asp	Cys	Arg	Ala	Asn	Leu	Ile	Val	Met	Pro
			35				40						45		
Leu	Leu	Ile	Leu	Phe	Glu	Ser	Met	Leu	Cys	Lys	Ile	Ile	Ile	Lys	Lys
			50				55						60		
Val	Ala	Tyr	Thr	Glu	Ile	Asp	Tyr	Lys	Ala	Tyr	Met	Glu	Gln	Ile	Glu
					70					75					80
Met	Ile	Gln	Leu	Asp	Gly	Met	Leu	Asp	Tyr	Ser	Gln	Val	Ser	Gly	Gly
					85				90					95	
Thr	Gly	Pro	Leu	Val	Tyr	Pro	Ala	Gly	His	Val	Leu	Ile	Tyr	Lys	Met
				100				105						110	
Met	Tyr	Trp	Leu	Thr	Glu	Gly	Met	Asp	His	Val	Glu	Arg	Gly	Gln	Val
				115				120					125		
Phe	Phe	Arg	Tyr	Leu	Tyr	Leu	Leu	Thr	Leu	Ala	Leu	Gln	Met	Ala	Cys
				130				135				140			
Tyr	Tyr	Leu	Leu	His	Leu	Pro	Pro	Trp	Cys	Val	Val	Leu	Ala	Cys	Leu
					150					155					160
Ser	Lys	Arg	Leu	His	Ser	Ile	Tyr	Val	Leu	Arg	Leu	Phe	Asn	Asp	Cys
				165					170					175	
Phe	Thr	Thr	Leu	Phe	Met	Val	Val	Thr	Val	Leu	Gly	Ala	Ile	Val	Ala
				180				185						190	
Ser	Arg	Cys	His	Gln	Arg	Pro	Lys	Leu	Lys	Lys	Ser	Leu	Ala	Leu	Val
				195				200					205		
Ile	Ser	Ala	Thr	Tyr	Ser	Met	Ala	Val	Ser	Ile	Lys	Met	Asn	Ala	Leu
				210				215					220		
Leu	Tyr	Phe	Pro	Ala	Met	Met	Ile	Ser	Leu	Phe	Ile	Leu	Asn	Asp	Ala
					230					235					240
Asn	Val	Ile	Leu	Thr	Leu	Leu	Asp	Leu	Val	Ala	Met	Ile	Ala	Trp	Gln
					245					250				255	
Val	Ala	Val	Ala	Val	Pro	Phe	Leu	Arg	Ser	Phe	Pro	Gln	Gln	Tyr	Leu
				260				265						270	
His	Cys	Ala	Phe	Asn	Phe	Gly	Arg	Lys	Phe	Met	Tyr	Gln	Trp	Ser	Ile
				275				280						285	
Asn	Trp	Gln	Met	Met	Asp	Glu	Glu	Ala	Phe	Asn	Asp	Lys	Arg	Phe	His

290	295	300
Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val		
305	310	315
Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His		320
	325	330
Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile		335
	340	345
Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg		350
	355	360
Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile		365
	370	375
Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr		380
385	390	395
Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala		400
	405	410
Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Leu Ala		415
	420	425
Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg		430
	435	440
Thr Thr Ser Ser Met Glu Lys Lys Leu Asn		445
450	455	

<210> 26

<211> 443

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> MOD_RES

<222> (333)...(347)

<223> Variable amino acid

<400> 26

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	20	25
Cys Lys Ile Ile Ile Lys Lys Val Ala Tyr Thr Glu Ile Asp Tyr Lys		30
	35	40
Ala Tyr Met Glu Gln Ile Glu Met Ile Gln Leu Asp Gly Met Leu Asp		45
	50	55
Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Gly		60
65	70	75
His Val Leu Ile Tyr Lys Met Met Tyr Trp Leu Thr Glu Gly Met Asp		80
	85	90
His Val Glu Arg Gly Gln Val Phe Phe Arg Tyr Leu Tyr Leu Leu Thr		95
	100	105
Leu Ala Leu Gln Met Ala Cys Tyr Tyr Leu Leu His Leu Pro Pro Trp		110
	115	120
Cys Val Val Leu Ala Cys Leu Ser Lys Arg Leu His Ser Ile Tyr Val		125
	130	135
Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr Leu Phe Met Val Val Thr		140
145	150	155
Val Leu Gly Ala Ile Val Ala Ser Arg Cys His Gln Arg Pro Lys Leu		160
	165	170
Lys Lys His Gln Thr Cys Lys Val Pro Pro Phe Val Phe Phe Phe Met		175

Cys	Ala	Ser	Tyr	Arg	Val	His	Ser	Ile	Phe	Val	Leu	Arg	Leu	Phe	Asn		
130						135			140								
Asp	Pro	Val	Ala	Met	Val	Leu	Leu	Phe	Leu	Ser	Ile	Asn	Leu	Leu	Leu		
145						150			155							160	
Ala	Gln	Arg	Trp	Gly	Trp	Gly	Cys	Cys	Phe	Phe	Ser	Leu	Ala	Val	Ser		
165						170									175		
Val	Lys	Met	Asn	Val	Leu	Leu	Phe	Ala	Pro	Gly	Leu	Leu	Phe	Leu	Leu		
180						185						190					
Leu	Thr	Gln	Phe	Gly	Phe	Arg	Gly	Ala	Leu	Pro	Lys	Leu	Gly	Ile	Cys		
195						200						205					
Ala	Gly	Leu	Gln	Val	Val	Leu	Gly	Leu	Pro	Phe	Leu	Leu	Glu	Asn	Pro		
210						215						220					
Ser	Gly	Tyr	Leu	Ser	Arg	Ser	Phe	Asp	Leu	Gly	Arg	Gln	Phe	Leu	Phe		
225						230			235							240	
His	Trp	Thr	Val	Asn													